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GenCore version 5.1.4-p5-4578
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1 protein - protein search, using sw model
  on: May 19, 2003, 16:41:42 ; Search time 56.5586 Seconds
      (without alignments)
  1362.510 Million cell updates/s

US-09-625-573-2
  perfect score: 1970
  sequence: 1 MLSTSRSRFIRNTNESGEERY.....GKGKSIGRAPEASLQDKEGA 374
  scoring table: BLOSUM62
  Gapop 10.0 , Gapext 0.5

  searched: 671580 seqs, 206047115 residues
  total number of hits satisfying chosen parameters: 671580

  minimum DB seq length: 0
  maximum DB seq length: 2000000000

  post-processing: Minimum Match 0%
                    Maximum Match 0%
                    Listing first 45 summaries
  SPTRNMBL 21:*
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SUMMARIES					
	Query No.	Score	Match Length	DB	ID
1:	1	1252	63.6	352	6 Q95NC2
2:	2	1244	63.1	339	6 Q9TUV8
3:	3	1244	63.1	339	6 Q9TQ3
4:	4	1244	63.1	352	6 Q9MZA0
5:	5	1243	63.1	339	6 Q9TQ5
6:	6	1243	63.1	352	6 Q9INC4
7:	7	1240	62.9	339	6 Q9TUW0
8:	8	1239	62.9	352	6 Q9MZZ9
9:	9	1238	62.9	339	6 Q9TUV6
10:	10	1238	62.8	339	6 Q9TUW1
11:	11	1237	62.8	339	6 Q9TUV9
12:	12	1236	62.7	339	6 Q9TQW0
13:	13	1235	62.7	339	6 Q9TRSN3
14:	14	1235	62.7	352	6 Q97776
15:	15	1234	62.7	339	6 Q9TUV5
16:	16	1233	62.6	339	6 Q9TUV2
17:	17	SP_Archeap:	*		

Q95ne1	cercocebus
Q9lux0	hylobates c
Q9tuv4	callithrix
Q9tuv5	atous trivi
Q9tut9	macaca mula
Q9tut9w	hylobates c
Q9xt12	cercopithec
Q95ic9	alouatta se
Q95nc0	hylobates m
Q9tut7w	pan troglod
Q9tut7	macaca fusc
Q9tut5	macaca mula
Q9tut4	macaca mula
Q9tut1	macaca mula
Q9tut1	pan troglod
Q9tq4	pongo pygma
Q9tq2	seguinus sp
Q9tq12	macaca nem
Q9tq1	macaca mula
Q9tq10	macaca fasc
Q95nc5	hylobates s
Q97975	macaca arct
Q9tut2	pan troglod
Q9tut6	colobus que
Q9tq3	cercopithec
Q9tav2	papio cyno
Q9tqr2	gorilla gor
Q18770	pan troglod
Q9tqv49	cercocebus

ALIGNMENTS

Result No.	Score	Query			DB	ID	Description
		Match	Length	ID			
1	1252	63 . 6	352	6	Q95NC2		Q95nc2 caliced
2	1244	63 . 1	339	6	Q9TUW8		Q9tuw8 saquinu
3	1244	63 . 1	339	6	Q9TQ73		Q9tqt3 callith
4	1244	63 . 1	352	6	Q9MZA0		Q9mza0 callith
5	1243	63 . 1	339	6	Q9TQV5		Q9tqv5 saquinu
6	1243	63 . 1	352	6	Q95NC4		Q95nc4 atelies '
7	1240	62 . 9	339	6	Q9TUW0		Q9tuw0 saquinu
8	1239	62 . 9	352	6	Q9MZ99		Q9mzz99 atelies :
9	1238 . 5	62 . 9	339	6	Q9TUW6		Q9tuw6 saquinu
10	1238	62 . 8	339	6	Q9TUW1		Q9tuw1 saquinu
11	1237	62 . 8	339	6	Q9TUW9		Q9tuw9 saquinu
12	1236	62 . 7	339	6	Q9TQW0		Q9tqw0 hyobat
13	1235	62 . 7	339	6	Q9TSN3		Q9tsn3 macaca
14	1235	62 . 7	352	6	Q97776		Q97776 cercocel
15	1233	62 . 6	339	6	Q9TUW5		Q9tuw5 saquinu
16	1233	62 . 6	339	6	Q9TUW2		Q9tuw2 alouatta

PRINTS; PRO0237; GPCRRIHODPSEN.	24	FDDYDG--APCHKEFDVKOIGAQALLPLPLSYLVLIFQPGVGNLNVLLINCKKLKCLTDIYL	81
PROSITE; PS00196; COPPER_BLOE; UNKNOWN_1.	:1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1		
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.	Db	YDDYGPSEPCRDKVQMGAHLLPPLSMVFLFGVGNLNVLLINCKRKPSMTDIYL	62
PROSITE; PS05262; G_PROTEIN_RECEP_F1_2; 1.			
Receptor.	KW		
SEQUENCE	SEQUENCE	352 AA: 40471 MW: 01E3972A87DB64D CRC64;	
Query Match	Best Local Similarity	62.9%; Score 1239; DB 6; Length 352;	
Best Local Matches	235; Conservative	76.3%; Pred. No. 2.1e-101; Mismatches 27; Indels 12; Gaps 3;	
Matches	235		
24	FDDYGA--PCHKEFDVKOIGAQALLPLPLSYLVLIFQPGVGNLNVLLINCKKLKCLTDIYL	81	
QY	:1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1		
10	YDDYGPSEPCRDKVQMGAHLLPPLSMVFLFGVGNLNVLLINCKRKPSMTDIYL	69	
Ddb			
82	LNLIAISDLFLITLPLWAHSAANEWVGNAQMCKLFTGLYHIGYFGIFFLTLTIDRYLA	141	
QY	:1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1		
70	LNLIAISDLFLITLPLWAHSAANEWVGNAQMCKLFTGLYHIGYFGIFFLTLTIDRYLA	129	
Ddb			
142	IYHAVEALKARTVTFGVVTSVITLVAVFASVPGTIFTKQKEDSYVVCGPYFPFRG----	197	
QY	:1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1		
130	IYHAVEALKARTVTFGVMSVITVWWVAVFASLPGTIFTKQREGHYTCSPHFPFQYQF	189	
Ddb			
198	WNNHTIMNHTIMNIGLYPLPLMIVCGILKTLLRGRNEKPKRPHRAYEVIFTIMIVFLWT	257	
QY	:1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1		
190	WKNFETLKVNLGVLVPLMIVCGILKTLLRGRNEKPKRHLIFTMIVFLWA	249	
Ddb			
258	PYNITVLLNFQEQQFGLSNBESTSQLDQATQVTETLGTMCCINPIIAYGEKERSLSF	316	
QY	:1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1		
250	PYNITVLLNFQEQQFGLSNBESTSQLDQATQVTETLGTMCCINPIIAYGEKFRYLL	309	
Ddb			
317	-----HIA 319		
QY			
Db	310 VFFQKHIA 317		
RESULT 9	RESULT 9		
Q9TUW6	Q9TUW6	PRELIMINARY; PRT; 339 AA.	
ID	ID	SEQUENCE FROM N.A.	
AC	AC	SEQUENCE FROM N.A.	
DT	DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
CDE	CDE	C-C chemokine receptor 5 (Fragment).	
GN	GN	CCR5.	
OS	OS	Saginus sp.	
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.	
NCBI_TaxID	NCBI_TaxID	100754;	
OX	OX	NCBI_TaxID=100754;	
RN	RN		
[1]	[1]		
RP	RP	SEQUENCE FROM N.A.	
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.; "Sequences of the CCR5 genes from diverse simian and prosimian species." Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.; "Sequences of the CCR5 genes from diverse simian and prosimian species." Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR	DR	PRINTS; PR0000923; GPCR_Rhodopsn.	
DR	DR	InterPro; IPR0000923; BlueCUC1.	
DR	DR	EMBL; AF161924; AAD47681.1.	
DR	DR	InterPro; IPR0000923; BlueCUC1.	
DR	DR	PRINTS; PR0000923; GPCR_Rhodopsn.	
DR	DR	InterPro; IPR0000923; BlueCUC1.	
DR	DR	PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.	
DR	DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.	
DR	DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.	
KW	KW	Receptor.	
FT	FT	NON_TER 1	
FT	FT	NON_TER 339	
SQ	SQ	SEQUENCE 339 AA; 39069 MW; 514623770BC70028 CRC64;	
Query Match	Best Local Similarity	62.8%; Score 1238; DB 6; Length 339;	
Matches	236; Conservative	76.6%; Pred. No. 2.5e-101; Mismatches 35; Indels 12; Gaps	
24	FDDYDG--APCHKEFDVKOIGAQALLPLPLSYLVLIFQPGVGNLNVLLINCKKLKCLTDIYL	81	
QY	:1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1		
Db	3 YDDYGPSEPCRDKVQMGAHLLPPLSMVFLFGVGNLNVLLINCKRKPSMTDIYL	62	
123	IYHAVEALKARTVTFGVMSVITVWWVAVFASLPGTIFTKQREGHYTCSPHFPFQYQF	18	
Query Match	Best Local Similarity	62.9%; Score 1238.5; DB 6; Length 339;	
Matches	238; Conservative	75.3%; Pred. No. 2.2e-101; Mismatches 26; Indels 9; Gaps 3;	
24	IYHAVEALKARTVTFGVVTSVITLVAVFASVPGTIFTKQKEDSYVVCGPYFPFRG----	19	
QY	:1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1 :1:1		
Db	63 LNLIAISDLFLITLPLWAHSAANEWVGNAQMCKLFTGLYHIGYFGIFFLTLTIDRYLA	122	

OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).	J. Exp. Med. 0:0-0(1998).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR AF04004; AAC2472.1;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	DR InterPro; IPR000276; GPCR_Rhodopsn.
OC	Cercopithecinæ; Macaca.	DR Pfam; PF00001; 7tm_1;
NCBI_TAXID=9541;	[1]	DR PRINTS; PR00237; GPCR_RHODOPSN.
RN		DR PROSITE; PS00231; G_PROTEIN_RECIP_F1_1;
RP	SEQUENCE FROM N.A.	DR PROSITE; PS50265; G_PROTEIN_RECIP_F1_2;
RA	Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,	DR Receptor.
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;	SEQUENCE 352 AA; 40475 MW; B3A63FDCA473D1D3 CRC64;
RT	"Sequences of the CCR5 genes from diverse simian and prosimian species";	Query Match 62.7%; Score 1235; DB 6; Length 352;
RT	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	Best Local Similarity 76.9%; Pred. No. 4.7e-101;
RL	EMBL; AF161951; AAD7707.1;	Matches 237; Conservative 27; Mismatches 32; Indels 12; Gaps 3;
DR	InterPro; IPR000276; GPCR_Rhodopsn.	KW
DR	PF00001; 7tm_1;	FT 24 FDYDY -GAPCHKFDYKQIGAQOLPPLPSLVFVGFVNMLUVVLLINCKKLKC1TDYL 81
DR	PRINTS; PR00237; GPCR_RHODOPSN.	DR 10 YDIDYTSEPCQKINVQIAARLPLPVSLVFVGFVNLLUVVLLINCKLKSM2DIYL 69
DR	PROSITE; PS00237; G_PROTEIN_RECIP_F1_1;	DR 82 LNLAISDLFLFLITPLWAHSAAANEVFGNAMCKLFPGLYHIGYFGGIFFFILLTIDRYLA 141
DR	PROSITE; PS50262; G_PROTEIN_RECIP_F1_2;	DR 70 LNLAISDLFLFLITPVWAHAAQWDFGNTNCQLLGLYFGFSGIFFFLITLIDRYLA 129
KW	Receptor.	DR 70 WNNFHFTMRNLLGVLPLLIINVTCYSGILKTLLCRNEKKRRAVRVIFTIMIVYFLFWT 257
FT	NON_TER 1	DR 142 IVHAYFAALKARTVTFGVTSVITWLVAVFASVPGTIFTKCQKEDSVYVCGPYFP ---RG 197
FT	NON_TER 339 339 MW; F0132E8BC44E8B29 CRC64;	DR 130 IVHAYFAALKARTVTFGVTSVITWLVAVFASVPGTIFTSREGLHYTCRNEKKRRAVRVIFTIMIVYFLFWT 257
SQ	SEQUENCE 339 AA; 39098 MW;	DR 190 WKNFQTLKIVTGLVEPLVWVTCYSGILKTLLCRNEKKRRAVRVIFTIMIVYFLFWA 249
Query Match 62.7%; Score 1235; DB 6; Length 339;	DR 198 WNNFHFTMRNLLGVLPLLIINVTCYSGILKTLLCRNEKKRRAVRVIFTIMIVYFLFWT 257	
Best Local Similarity 77.3%; Pred. No. 4.5e-101;	DR 258 PYNTIVLLNTPEFFGLSNCESTSOLDQATOVTETGMTHCCINPIIYAFVGKFRFLF- 316	
Matches 238; Conservative 25; Mismatches 33; Indels 12; Gaps 3;	DR 250 PYNTIVLLNTPEFFGLSNCSSNRQAMOVTETGMTHCCINPIIYAFVGKFRNYLL 309	
QY	24 FDYDY -GAPCHKFDYKQIGAQOLPPLPSLVFVGFVNMLUVVLLINCKKLKC1TDYL 81	DR 317 --- HIA 319
Db	3 YDIDYTSEPCQKIDVKQTAARLPLPVSLVFVGFVNLLUVVLLINCKLKSM2DIYL 62	Db 310 VFFQKHIA 317
QY	82 LNLAISDLFLFLITPLWAHSAAANEVFGNAMCKLFPGLYHIGYFGGIFFFILLTIDRYLA 141	RESULT 15
Db	63 LNLAISDLFLFLITPLWAHSAAANEVFGNAMCKLFPGLYHIGYFGGIFFFILLTIDRYLA 122	Q9TUV5 PRELIMINARY; PRT; 339 AA.
QY	142 IVHAYFAALKARTVTFGVTSVITWLVAVFASVPGTIFTKCQKEDSVYVCGPYFP ---RG 197	AC Q9TUV5
Db	123 IVHAYFAALKARTVTFGVTSVITWLVAVFASLSPGLITRSOREGLHYTCSSHFPYSQYQF 182	AC Q9TUV5 PRELIMINARY; PRT; 339 AA.
QY	198 WNNFHFTMRNLLGVLPLLIINVTCYSGILKTLLCRNEKKRRAVRVIFTIMIVYFLFWT 257	DT 01-MAY-2000 (TREMBLrel. 13, Created)
Db	183 WKNFQTLKIVTGLVEPLVWVTCYSGILKTLLCRNEKKRRAVRVIFTIMIVYFLFWA 242	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
QY	258 PYNTIVLLNTPEFFGLSNCESTSOLDQATOVTETGMTHCCINPIIYAFVGKFRFLF- 316	DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
Db	243 PYNTIVLLNTPEFFGLSNCESTSOLDQATOVTETGMTHCCINPIIYAFVGKFRNYLL 302	DE C-C chemokine receptor 5 (Fragment).
QY	317 --- HIA 319	GN Saguinus sp.
Db	303 VFFQKHIA 310	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus OC NCBI_TAXID=100754;
OX		OX NCBI_TAXID=100754;
RN		OX
RP		RP SEQUENCE FROM N.A.
RP		RP Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RP		RP "Sequences of the CCR5 genes from diverse simian and prosimian RT species";
RP		RP Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RP		DR EMBL; AF161933; ADD4790.1;
RP		DR InterPro; IPR000276; GPCR_Rhodopsn.
RP		DR Pfam; PF00001; 7tm_1;
RP		DR PRINTS; PR00237; GPCR_RHODOPSN.
RP		DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
RP		DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1;
RP		DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2;
RP		DR Receptor.
RC	SEQUENCE FROM N.A.	FT NON_TER 1 1
RC	STRAIN=1:208;	FT NON_TER 339 339 MW; 8DACBDD06C785073 CRC64;
RA	Chen Z., Kwon D., Jin Z., Monard S., Teifter P., Jones M., Lu C., Aguilal R., Ho D.D., Marx P.A.;	FT SQ 339 AA; 39021 MW; 8DACBDD06C785073 CRC64;
RT	"Natural infection of a homozygous delta 24 CCR5 red-capped mangabey with a R2b-tropic simian immunodeficiency virus.";	Query Match 62.6%; Score 1234; DB 6; Length 339;

	Best Local Similarity	Conservative	Pred.	No.	5.5e-101;	Matches	Mismatches	35;	Indels	12;	Caps	3;
Qy	24	FDYDGG--	-A	CHKEFVKQKQIAQQLPPLYSVAVIFSPGVNMIVVLLI	NCKLKCLTDYL	81						
Db	3	YDIDYGPSEC	RKIDVKQMAHLLPPLYSVAVFLFGVGNMIVVLLI	NCRPKSMUDYL	62							
Qy	82	LNLATSDLILFLITLPLW	AHSAAENWVFGNAMCKLEPTGLYHIGYFGGIFTILLTDRYLA	141								
Db	63	LNLATSDLILFLITL	PLW	AHSAAENWVFGNAMCKLEPTGLYHIGYFGGIFTILLTDRYLA	141							
Qy	142	IYHAFALKARTVTF	GVVTSVITLVA	VPSVPGLIIFTKCQEDSVVCGPYFPRO	--	197						
Qy	142	IYHAFALKARTVTF	GVVTSVITLVA	VPSVPGLIIFTKCQEDSVVCGPYFPRO	--	197						
Db	123	IYHAFALKARTVTF	GVVTSVITLVA	VPSVPGLIIFTKCQEDSVVCGPYFPRO	--	197						
Qy	198	WNNHTIMNTLIGVPL	LLIVCYSGILKTLR	CRNEKKHRAYRVFTIMITYFLFWT	257							
Db	183	WKNFETLKMV	VLGVLVPLLIMIVCYSGILKTLR	CRNEKKHRAYRVFTIMITYFLFWT	242							
Qy	258	PYNVILLINT	QEFFGLSNCE	ESTSQLDAQTQVTTLGMTHCINPITYA	YGEKERSLF-	316						
Qy	243	PYNVILLINT	QEFFGLSNCE	ESTSQLDAQTQVTTLGMTHCINPITYA	YGEKERSLF-	316						
Qy	317	---	HIA	319								
Db	303	VFFQKHIA	310									

Search completed: May 19, 2003, 16:48:11
 Job time : 57.5586 secs